FIG. 1A

Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

```
GTCGACCCACGCGTCCCACTCAACAATGCCTGCCCCTCTCTGACTGCACCGTCCCGCGCCGTCCCGGCGCGCC          79

CAAGCCAAGTGCGAGCGGGGGCGTTGCCCACCGACACAGCCCTTGGCCCCGCCCGGACCAGGAGGTGAGCCGGCGCG      158

                                                    M   H   S   G   S   P
CGCACAGCTCCGTGCGCTCGCCCGTCTGAGCGCCGCCAGGTGCCCGCCAGTGCCCGCCGGAGATGCACAGCGGCAGCCCG    4
                                                                              233

P   G   L   L   A   L   W   L   C   A   V   L   C   A   S   A   R   G   G   S
CCTGGGCTCCTGGCGCTGTGGCTTTGCGCTGTGCTGTGCGCATCGGCGCGCGGGGGCAGC                          24
                                                                              293

D   P   Q   P   G   P   R   P   A   C   P   A   P   C   H   C   Q   E   D
GACCCCCAGCCTGGCCCGGGGCGTCCCGCCTGCCCCTGCGCTCCCTGCCACTGCCAGGAGGAC                       44
                                                                              353

G   I   M   L   S   A   D   C   S   E   L   G   L   S   V   V   P   A   D   L
GGCATCATGCTGTCCGCTGACTGCTCCGAGCTCGGGCTCTCAGTGGTGCCTGCGGACCTG                          64
                                                                              413

D   P   L   T   A   Y   L   D   L   S   M   N   N   L   T   E   L   Q   P   G
GACCCCCTGACGGCTTACCTAGACCTCAGTATGAACAACCTCACGGAGCTTCAGCCGGGT                          84
                                                                              473

L   F   H   L   R   F   L   E   E   L   R   L   S   G   N   L   S   H   L   H
CTCTTCCACCTGCGCTTCCTGGAGGAGCTGCGGCTCTCAGGGAACCTCTCACAC                               104
                                                                              533

I   P   G   Q   A   F   S   G   L   H   S   L   K   L   I   L   M   Q   S   N
ATCCCGGGACAGGCATTCTCCGGCCTCCACAGCCTCAAAATTCTAATGCTGCAGAGCAAC                         124
                                                                              593
```

FIG.1B

```
Q   L   R   G   I   P   A   E   A   L   W   E   L   P   S   L   Q   S   L   R      144
CAG CTC CGT GGG ATC CCA GCA GAG GCA CTA TGG GAG CTG CCC AGC CTG CAG TCG CTG CGC    653

L   D   A   N   L   I   S   N   V   L   P   E   F   S   E   G   L   S   S   L      164
CTA GAT GCT AAT CTC ATC TCC AAT GTC CTG CCT GAG TTT AGC GAG GGG CTC TCC TCC CTC    713

R   H   A   W   L   L   D   D   N   A   T   E   I   H   H   R   A   N   D   N      184
CGC CAC GCC TGG CTC CTC GAT GAC AAT GCA ACT GAG ATC CAT CAT CGC GCT AAC GAC AAC    773

L   P   A   L   Q   A   M   T   S   I   L   V   L   G   E   N   I   P   D   Y      204
CTT CCT GCC CTA CAG GCC ATG ACC AGT ATC TTG GTG CTG GGG GAG AAC ATC CCT GAC TAT    833

A   F   Q   N   L   I   S   E   K   V   L   H   L   H   N   N   R   I   Q   H      224
GCC TTC CAG AAT CTC ATC AGT GAG AAA GTG CTG CAT CTA CAT AAC AAC CGC ATC CAG CAT    893

V   G   H   E   L   G   E   L   G   L   R   N   E   T   L   L   D   N   Y   N      244
GTG GGG CAC GAG CTG GGG GAG CTG GGG CTA AGG AAT GAG ACA CTA CTG GAC AAC TAT AAT    953

E   L   Q   E   F   S   L   G   A   L   L   L   L   G   L   Q   Q   L   G   F      264
GAG CTG CAG GAG TTC AGC CTG GGC GCA CTG AGG AGG CTG GGC CTG CAG CAG TTG GGT TTC   1013

H   N   N   I   K   A   F   E   M   P   T   K   A   F   G   G   N   L   L   Q      284
CAT AAC AAC ATC AAG GCT TTC GAG ATG CCA ACC AAA GCC TTC GGC GGC AAC CTC CTC CAG   1073

T   I   H   F   Y   D   N   P   I   Q   F   V   G   R   S   R   F   Q   Y   L      304
ACA ATA CAT TTT TAC GAC AAC CCA ATC CAG TTT GTG GGA AGG TCA AGG TTC CAG TAC CTG   1133
```

FIG. 1C

```
S    K    L    H    T    L    S    L    N    G    A    T    D    I    Q    E    F    P    D    L     324
TCT  AAA  CTG  CAT  ACG  CTA  TCT  TTG  AAT  GGT  GCC  ACT  GAT  ATC  CAA  GAG  TTC  CCA  GAC  CTC   1193

K    G    T    T    S    L    E    I    L    L    T    L    R    A    G    I    R    L    L    P     344
AAA  GGC  ACC  ACT  AGC  CTG  GAG  ATC  CTG  CTG  ACC  CTG  CGT  GCG  GGC  ATC  AGA  CTG  CTC  CCA   1253

P    G    V    C    Q    Q    L    P    I    E    E    I    L    E    L    S    H    N    Q    I     364
CCG  GGA  GTG  TGC  CAA  CAG  CTG  CCT  ATC  GAA  GAA  ATC  CTG  GAG  CTG  TCT  CAT  AAT  CAG  ATC   1313

E    E    L    P    S    L    H    R    E    L    K    L    E    E    E    G    L    R    H    N     384
GAG  GAG  TTA  CCC  AGC  CTG  CAC  AGA  GAG  CTG  AAG  CTG  GAG  GAA  GAG  GGC  CTC  CGA  CAT  AAC   1373

R    I    K    E    I    G    A    D    I    G    S    Q    S    G    L    S    Q    A    L    D     404
AGG  ATC  AAG  GAA  ATT  GGT  GCA  GAT  ATT  GGC  TCC  CAA  TCC  GGC  TTG  TCC  CAA  GCT  TTA  GAC   1433

L    S    W    N    A    I    R    A    E    H    P    E    S    F    S    T    L    R    S    L     424
CTG  AGT  TGG  AAT  GCC  ATC  CGT  GCC  GAA  CAC  CCT  GAG  TCA  TTC  TCA  ACC  CTT  CGA  TCC  TTG   1493

V    K    L    D    L    T    D    N    L    A    L    T    L    P    L    A    A    L    G    G     444
GTT  AAG  CTG  GAC  CTG  ACT  GAC  AAC  CTG  GCC  CTG  ACA  CTG  CCC  CTG  GCT  GCT  CTG  GGA  GGC   1553

L    M    H    L    K    L    K    G    N    A    L    A    S    Q    Q    F    S    K    D    S     464
CTG  ATG  CAC  CTC  AAG  CTC  AAG  GGG  AAC  GCC  TTG  GCC  TCT  CAG  CAG  TTC  TCC  AAG  GAC  AGT   1613

F    P    K    L    R    L    I    R    V    Y    P    A    Y    Q    Q    C    A    Y    G    I     484
TTC  CCA  AAA  CTG  AGG  CTG  ATC  AGG  GTG  TAC  CCC  GCC  TAC  CAG  CAG  TGT  GCC  TAC  GGC  ATC   1673
```

FIG.1D

```
C   A   S   F   F   K   T   S   G   Q   Q   W   Q   A   E   D   F   H   P   E   E        504
TGT GCC AGC TTC TTC AAG ACC TCT GGG CAG CAG TGG CAG GCC GAG GAC TTT CAT CCA GAA GAA     1733

E   E   A   P   K   R   L   Q   L   L   G   L   E   K   Q   A   E   N   P   H   Y   D    524
GAG GAG GCA CCA AAG AGG CTC CAG CTT CTT GGA CTC CTG AAG CAA GCT GCC GAG AAC CAC TAT GAC 1793

L   D   L   D   V   P   G   L   K   S   D   D   P   F   L   Q   S   S   V   Q            544
CTA GAC CTG GAT GTT CCT GGC CTG AAG TCA GAC GAC CCA TTT CTC CAA TCA AGT GTC CAG         1853

C   S   P   V   W   G   P   K   L   L   P   V   V   C   H   L   E   S   G   I            564
TGC AGC CCT GTT TGG GGC CCC AAG CTG CTC CCC GTC GTA TGT CAC CTC GAG AGC GGC ATC         1913

R   L   A   V   W   A   S   P   L   K   V   P   L   G   L   V   V   V   L   L            584
CGC CTT GCT GTG TGG GCC AGC CCG CTG AAG GTC CCC CTG GGG CTG GTG GTG GTG CTG CTG         1973

T   V   F   A   G   S   G   L   C   K   N   L   A   S   V   V   D   A   M                604
ACA GTC TTT GCC GGA AGC GGA CTG TGT AAG AAC CTT GCC TCT GTG GTG GAC GCG ATG             2033

A   G   A   N   A   L   S   I   G   C   L   L   S   A   L   G   W   D   A   L            624
GCA GGC GCC AAC GCC CTG TCC ATT GGC TGT CTC CTG TCT GCC CTG GGT TGG GAC GCC TTG         2093

T   G   Y   E   A   F   Q   G   Y   G   W   A   R   E   A   S   E   A   S   A            644
ACC GGT TAT GAG GCT TTC CAG GGT TAT GGA TGG GCC CGC GAG GCC AGC GAG GCG TCG GCT         2153

T   G   F   L   A   V   V   L   L   L   L   T   L   G   A   A   A   A   A                664
ACG GGC TTC CTG GCT GTC GTC CTG CTG CTG CTG ACA CTG GGT GCG GCC GCC GCG GCC             2213
```

FIG. 1E

```
V   Q   C   S   I   V   T   C   V   A   R   A   Y   G   K   A   P   S   P   G        684
GTG CAG TGC AGC ATC GTG ACC TGC GTC GCC CGA GCC TAC GGG AAG GCG CCG TCG CCT GGC      2273

S   V   R   S   A   A   G   I   G   L   G   V   S   A   L   A   L   A   A   P        704
AGC GTC CGC TCG GCA GCA GGC ATC GGC CTG GGG GTG AGT GCC CTG GCG CTG GCA GCA CCG      2333

L   A   S   V   G   E   Y   G   F   G   F   I   K   Y   L   Y   C   L   Y   A        724
CTG GCC TCG GTG GGC GAG TAT GGC TTC GGC TTC ATC AAG TAC CTC TAC TGT CTC TAC GCC      2393

G   R   P   A   A   A   A   L   G   F   A   A   Y   V   A   A   L   S   L   C        744
GGC CGG CCG GCC GCC GCC GCC CTG GGC TTC GCT GCT TAC GTA GCC GCC CTG TCG CTC TGC      2453

L   V   V   A   G   A   A   Y   L   Y   L   Q   L   D   F   D   G   D   F   E        764
CTG GTG GTG GCC GGC GCC GCC TAC CTC TAC CTC CAG CTG GAC TTT GAC GGT GAC TTT GAG      2513

A   V   W   D   C   A   M   A   F   V   H   A   W   M   S   L   G   F   A   D        784
GCC GTG TGG GAC TGC GCC ATG GCC TTT GTG CAC GCG TGG ATG TCC CTC GGC TTT GCA GAT      2573

L   C   C   P   V   F   F   L   S   F   F   A   L   L   G   L   F   P   V   T        804
CTC TGC TGC CCC GTG TTC TTC CTC AGC TTT TTT GCC CTG CTC GGC CTC TTC CCT GTC ACC      2633

P   E   A   V   V   K   V   S   V   L   L   V   V   L   P   P   L   L   A   C        824
CCC GAG GCT GTC GTC AAG GTC TCA GTC CTT CTT GTG GTG CTG CCT CCT CTG CTG GCC TGC      2693

L   Y   Y   L   L   F   N   P   H   F   R   D   D   R   L   D   L   R   L   W        844
CTG TAC TAC CTC CTC TTC AAC CCT CAC TTC CGG GAT GAT CGG CTT GAC CTC CGG CTG TGG      2753
```

FIG. 1F

```
     P   R   S   P   G   P   L   A   Y   A   A   A   G   E   L   E   E   K   S   S   C    864
     CCT CGG TCC CCA GGG CCC CTA TAC GCC GCA GCC GGT GAG CTG GAG AAG AGC TCC TGC        2813

     D   S   T   Q   A   L   V   A   F   S   D   V   D   L   I   I   E   L   I   S   E    884
     GAC TCC ACC CAA GCG CTG GTG GCT TTC TCA GAT GTG GAT CTT ATT CTG GAA GCT TCT GAG    2873

     A   G   Q   Q   P   P   L   E   T   Y   G   F   P   S   V   T   L   I   S   R    904
     GCT GGG CAG CAG CCT CCT GGG CTA GAG ACC TAT GGC TTC CCT TCA GTG ACC CTC ATC TCC CGA    2933

     H   Q   P   G   A   T   R   L   E   G   N   H   F   I   E   S   D   G   T   K    924
     CAT CAG CCG GGG GCC ACC AGG CTG GAG GGA AAC CAT TTT ATA GAG TCT GAT GGA ACC AAG    2993

     F   G   N   P   Q   P   P   M   K   G   E   L   L   L   K   A   E   G   A   T    944
     TTT GGG AAC CCA CAA CCT CCC ATG AAG GGA GAA CTG CTG CTG AAG GCA GAG GGA GCC ACT    3053

     L   A   G   C   G   S   S   V   G   G   A   L   W   P   S   G   S   L   F   A    964
     TTG GCA GGC TGT GGC TCT TCC GTG GGT GGA GCC CTC TGG CCC TCT GGC TCT CTC TTT GCC    3113

     S   H   L   *                                                                   968
     TCT CAC TTG TAA                                                                 3125

ATAATCCCTCTCTGTTTGTCCTCTCCCATCCAATGATGGCTGCTTATAAAAGAAAGACAACTCCAACTCCATAGCAAGA    3204

TGGCCAACACCTTCTGACTCCATTGTTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGCTTGTCTTGG      3283

CCTTCAGCTTCACTTTCACCCTGGGCCTTCTCTGTCCAATCCAATACTTCTGACAGAGAGGCCTGGGAAATTTGCATAGGA   3362
```

FIG.1G

```
GAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGCCCTGACAGAGCCATGATCAGTAAGTGCAGAGTGATGGGGAG    3441

GTCTCACAGAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTGTGACATATAGAATATAAAATG    3520

TGTTCTGCGTTCCATTAATCTTGACCTATGCTGNGCCAAAGTGCTTCCTGTTAAAATACACTTTGGAAGACATTGAAAA    3599

AAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC    3637
??
```

FIG. 2A

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
```
              *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
                +LdLs N+Lt+l pg++++L+ LeeL Ls+N+L+++p ++f++L+
ftmzb048h1
         67   LTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH   114
```

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
```
              *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
                +L+ L L+ N+L++++p++al+ Lp+L++L L+ N ++ +p+++f++L+
ftmzb048h1
         115  SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS  162
```

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
```
              *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
                +L++L+L++N Lt++p  al+nLp L+  L N++++++p++fqnL+
ftmzb048h1
         163  SLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT  210
```

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
```
              *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL k<-*
                +L +L+L nN+++++ +++++L+nLe+LdL++N+L+++p + + L+
ftmzb048h1
         211  SLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFPL-AIRTLG  257
```

FIG.2B

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
```
            *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
               +L+eL + nN+++ +p+ a+ + p L+++++ +N ++ +  ++fq L+
ftmzb048h1
        258   RLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS 305
```

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
```
            *->nLeeLdLsnNk.LtslppgalsnLpnLeeLdLsnNnLtslppglfqn Lk<-*
               +L++L+L++ +++++p+  l++ ++Le L L + ++ lppg++q L+
ftmzb048h1
        306   KLHTLSLNGATdIQEFPD--LKGTTSLEILTTRAGIRLLPPGVCQQLP 352
```

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
```
            *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
               +L+ L+Ls+N+++++lp+ l+ +++Lee+ L +N++++++ +++f+ L+
ftmzb048h1
        353   RLRILELSHNQIEELPS--LHRCQKLEEIGLRHNRIKEIGADTFSQLG 398
```

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
```
            *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
               +L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp + +L
ftmzb048h1
        399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLM 446
```

FIG. 3A-1

Protein (species)*	Function-ligand	Location
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm
Leucine-rich α2-GP (human)	?-?	Serum
RNA1 (Saccharomyces cerevisiae)	RNA processing-?	Cytoplasm
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus
Biglycan (human)	ECM binding-laminin, fibronectin, TGF-β	ECM
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin, TGF-β	ECM
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM
Lumican (chicken)	Corneal transparency-?	ECM
Proteoglycan-Lb (chicken)	?-?	ECM
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM
Platelet GP ba (human)	Cell adhesion-WF, thrombin	PM (EC)
Platelet GP V (human)	Cell adhesion-GP IX, GP 1b	PM (EC)
YopM (Yersinia pestis)	Virulence factor-thrombin	IC + EC
IpaH7.8 (Shigella flexnen)	?-?	?
IpaH4.5 (Shigella flexnen)	?-?	?
Toll (Drosophilla)	Embryo development-?	PM (EC)
Silt (Drosophilla)	Axon development-?	EC
Connectin (Drosophilla)	Synapse development-?	PM (EC)
Chaoptin (Drosophilla)	Photoreceptor-cell development-?	PM (EC)
Flightless-1 (Drosophilla)	Embryo development-?	PM (EC)
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)

FIG. 3A-2

Repeats	Length		Consensus sequence	PIR entry
			5 10 15 20 25	
15	28	(A)	.LE.L.L..C-.LT...C..L..aL....	A31857
	29	(B)	.L.EL.L..N-.LGD.Ga..L...L.P..	
8	24		.L.L.L..N-.L...-L....---	NBHUA2
8	29		.L.L.L..N-.L...a....a....	BVBYN1
4	24		.L.L.a..N-.a.....-....L--	S03616
8	24		.L.L.L..N-.I...-a.....a..---	A40757
10	24		.L.L.L..N-.I..-V....a..--	NBHUC8
11	24		.L.L.L..N-.a...-a....a..--	S05390
12	24		.L.L.L..N-.L...-......a..--	A41748
6	24		.L.a.L..N-.I.....-a.....--	A41781
6	24		.L.a.L..N-.a...-.....F.--	A35272
7	24		.L.L.L..N-.L..-LP.GL...L--	NBHUIA
14	24		.L.L.L..N-.L..-LP.LF.L--	-
12	20		.L.L.a..N-.L..-LP-.--L--PP	A33950
6	20		.L.V..N-.L..-LP-.----L--P.	A35149
8	20		.L.L.a..N-.L..-LP-.----L--P.	S18248
19	24		.L.L.L..N-.L...-....F..--	A29943
19	24		.L.L.L..N-.I...-....F.L--	A36665
7	24		.L.INL..N-.I...-a...aF.L--	S28464
30	24		.L.L.L..N-.a..-aP.a...F.a--	A29944
16	23		.L.L.LS.N-.L..-aP.a..-L--	-
8	24		.L.L.LSNN-.a...-a.....L---	A34210

FIG. 3B-1

Protein (species)*	Function-lgand	Location
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)
Trk (human)	Receptor protein kinase-NGF	PM (EC)
TrkB (mouse)	Receptor protein kinase-BDNF,	PM (EC)
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)
TMK1 (Arabidopsis thaliana)	Receptor protein kinase-?	PM (EC)
LH-CG receptor (rat)	Signal transduction-LH, CG	PM (EC)
PSH receptor (rat)	Signal transduction-PSH	PM (EC)
TSH receptor (dog)	Signal transduction-TSH	PM (EC)
Adenylate cyclase (Saccharomyces Cerevisiae)	Signal transduction-RAS	PM (cytoplasm)
T-LR (Typanosoma brucei)	?-?	?
RAD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	Nucleus
RAD7 (Saccharomyces cerevisiae)	DNA repair-?	?
DRT100 (Arabidopsis thallana)	Recombination-?	Chloroplast
GRR1 (Saccharomyces cerevisiae)	Signal transduction-?	Cytoplasm
CCR4 (Saccharomyces cerevisiae)	Transcription-?	?
sds22 (Schizosaccharomyces pombe)	Mitosis-dis2, sds21	Nucleus
p34 ribosome-binding protein(rat)	RM membranes-ribosome	RM membrane (cytoplasm)
Carboxypeptidase N (human)	Stabilization-catalytic subunit	Plasma
Intermalin (Listeria monocytogenes)	Invasion-?	Cell wall
IniB (Listeria monocytogenes)	?-?	?

LRR superfamily

FIG. 3B-2

Repeats	Length	Consensus sequence	PIR entry
8	27	.a..L.L.N-.............	TDHUM4
2	23	.L..L.LS.N-.L...-......--.	TVHUTT
3	23	.L.L.aT.N-.LTS..-....--T	S06943
3	23	.LR.aNLSQN-.L...S.-...--.	A40026
11	23	.L..a.L.N-...G.aP-.a-.SL--.	JQ1674
5	25	.L..L.a.T-.a.......F.--.	A41343
7	25	.L..L.aS.T----.LP..a..a--.	A34548
6	25	.a..L.a.NN..a.S-a....a..--.	A40077
20	23	.L..L.L..N-.a..-a..L--.	0YBY
18	23	.L..L.LSGC.a..--a..-a..L--.	A36359
3	23	.a.LàDI..N--LP..a.....N--.	DDBYD1
5	26	.L..L.a..C..a.....a...a...--P	A25226
5	24	.L..LNL..N-.L.G.IP.S-a.S.--.	A46260
9	26	.L..a.L.C.NaTD.a.--L.L.--.	A41529
4	23	.L..L.a..N-.LT.--LP.E-a...--.	S31286
11	22	.L..L.a..N-.I...-a--ENa..L--.	A38439
4	24	.L..LDL..N-.L..-LP...F.L--.	---
12	24	.L..L.L..N-.L.-.LP..aF..L--.	A34901
13	22	NL..L.L..n-QISDI.P--L..L--T	A39930
6	22	.L..L.L.N-.L.DI..---L..L--.	C39930
		5 10 15 20 25	
		.L..L.L..N*.a..*a****a**a**.**	

FIG. 4

>human DNA seq.
TAATACGACTCACTATAGGGAAAGCTGGTACGCCTG AGGTACCGGTCCGGAA
TTCCCGGGTCGACCCACGCGTCCGTGGAGCGGAGC CAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCCTC CAACACAACCGCATCTG
GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCTI CCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGC CCTTCTCCACCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTC ACCACACTGCCCCTGGC
TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGC GAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGA TCCTGGAGGTGCCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCT TCTTCAAGGCCTCTGGG
CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAC GAGTCTTCAAAAAGGCC
CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTA TGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACAC CCAGTGTCCAGTGTAGC
CCTACTCCAGGCCCCTTCAAGCCCTGTGAGTGACCTC TTTGAAAGCTGGGGCAT
CCGCCTGCCGTGTGGGCCATCGTGTTGCTCTCCG GCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCCC CTGCCCCCGGTCAAGTTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACI GGCATTTCCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTC TCTGAGTACGGAGCCC
GCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGC TTCCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCG CAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCC CTCCCTGGGCAGCGTTCG
AGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGC TGGCCGCCGCACTGCCC
CTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTC TGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT
GAACTCCTTCTGTTTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGA
CCTGCCGCGGGGCGACTTTGAGGCCGTGTGGGACI GCGCCATGGTGAGGCAC
GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTA(TGTCCCGTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCAC GCCCGAGGCCGTCAAGT
CTGTCCTGCTGGTGGTGCTGCCCCCTGCCTGCCTGC(TCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGGCCCCGCGC
AGGGGACTCAGGGCCCCTAGCCTATGCTGCGGCCCGGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTG
GAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC
AGTGACCCTCATCTCCTGTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGC
CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCTCCATGGA
TGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTG
TCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTGTA
AATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCC TTCCTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCAT
CACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCT
TGATACTGGGCCTCTTCCTTGTCATGTCTGAAGCTG1GGACCAGAGACCTGGAC
TTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGG
TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATT
AAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGT
GCATGCGACGTCATAGCTCTTCTATAGTGTCACCTAAATTCAATT

FIG. 5

>fahr human

NTTHYRESWYACRYRSGIPGSTHASVERSQGLSLPAHPASLAALAASNTTASGKLE
DTFSQLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD
DEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYL
FESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCG
LLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSEASVLLLTLAAVQCSVSVS
CVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQP
AALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLR
RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL
SGGGGFQPSGLAFASHV

FIG. 6

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11

```
        *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL
          +L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp  + +L
fahr  64  SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGL 110

          k<-*

fahr  111 M   111
```

FIG. 7A

```
                         1                                                                    80
ftmzb048h10              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               MHSPGLLALWLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSADCSELGLSVVPADLLPLTAYLDLSMNNLTE

                         81                                                                   160
ftmzb048h10              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               LQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLHSLKIIMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSPEG

                         161                                                                  240
ftmzb048h10              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               LSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLD

                         241                                                                  320
ftmzb048h10              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Aa_of_aambb001d112       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human               LNYNELQEFPPLAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLCQTIHFYDNPIQFVGRSAFQYLSKLHTLSLNGATDIQE

                         321                                                                  400
ftmzb048h10              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
Aa_of_aambb001d112       -----------NTTHYRES------WYACRYRS-----GIPGST--
fahr_human               FPDLKGTTSLEILTLTRAGIRLLPPGVCQQLPRLRILELSHNQIEELPSLHRCQKLEIGLRHNRIKEIGADTFSQLGSL

                         401                                                                  480
ftmzb048h10              ---H--ASVE-----RSQGLSLP-----AHPASLAALAASNTTASG-------------KLEX------------DTFSQLSSL
Aa_of_aambb001d112       QALDLSWNAIRAIHPEAFSTLRSIVKLDLTDNQLTTLPLAGLGIMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC
Fahr_human               QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGIMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC

                         481                                                                  560
ftmzb048h10              AYGICASFFKTSGQWQAEDFHPEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNFSVQCSPVPGPFKPCEHLFE
Aa_of_aambb001d112       AYGICASFFKTSGQWQAEDFHPEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPHPSVQCSPVPGPFKPCEHLFE
fahr_human               PYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYLFE
```

FIG. 7B

561   640

ftmzb048h10   SWGIRLAVWAIVILLSVLCNGLVLLIVFASGPSPLSPVKLVVGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGL
Aa_of_aambb001d112   SWGIRLAVWAIVILLSVLCNGLVLLIVFASGPSPLSPVKLVVGAMAGANALSGISCGLLASVDALTYGQFAEYGARWESGL
fahr_human   SWGIRLAVWAIVILLSVLCNGLVLLIVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGL

                             I   TM II

641   720

ftmzb048h10   GCQATGFLAVLGSEASVLLILAAVQCSISVTCVRAYGKAFSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY
Aa_of_aambb001d112   GCQATGFLAVLGSEASVLLILAAVQCSISVTCVRAYGKAFSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY
fahr_human   GCRATGFLAVLGSEASVLLILAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPY

                       TM III   TM IV

721   800

ftmzb048h10   APPEGRPAALGFAVALVMMNSLCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL
Aa_of_aambb001d112   APPEGRPAALGFAVALVMMNSLCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL
fahr_human   APPEGQPAALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL

                             TM V   TM VI

801   880

ftmzb048h10   FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
Aa_of_aambb001d112   FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
fahr_human   FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL

                       TM VII

881   960

ftmzb048h10   EASEAGQPPGLETYGFPSVTLISRHQPGATRLEGNHFIESDCTKFGNPQPPMKGELLLKAEGATLAGCCGSSVGGALWPSG
Aa_of_aambb001d112   EASEAGQPPGLETYGFPSVTLISRHQPGATRLEGNHFVESDGTKFGNFQPPMKGELLLKAEGATLAGCGSSVGGALWPSG
fahr_human   EASEAGRPPGLETYGFPSVTLISCQPGAPRLEGSHCVEPEGNHFGNFQPSMDGELLLRAEGSTPAGGGLSGGGFQPSG

961   968

ftmzb048h10   SLFASHLN
Aa_of_aambb001d112   SLFASHLN
fahr_human   LAFASHVN

FIG.8A

```
      G   L   H   N   L   E   T   L   D   L   N   Y   N   K   L   Q   E   F   P   V
      GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAT TAT AAC AAG CTG CAG GAG TTC CCT GTG    20
                                                                                          60

      A   I   R   T   L   G   R   L   Q   E   L   G   F   H   N   N   N   I   K   A
      GCC ATC CGG ACC CTG GGC AGA CTG CAG GAA CTG GGG TTC CAT AAC AAC AAC ATC AAG GCC    40
                                                                                         120

      I   P   E   K   A   F   M   G   N   P   L   L   Q   T   I   H   F   Y   D   N
      ATC CCA GAA AAG GCC TTC ATG GGG AAC CCT CTG CTA CAG ACG ATA CAC TTT TAT GAT AAC    60
                                                                                         180

      P   I   Q   F   V   G   R   S   A   F   Q   Y   L   P   K   L   H   T   L   S
      CCA ATC CAG TTT GTG GGA AGA TCG GCA TTC CAG TAC CTG CCT AAA CTC CAC ACA CTA TCT    80
                                                                                         240

      L   N   G   M   A   D   I   Q   E   F   P   D   L   K   G   T   T   S   L   E
      CTG AAT GGT ATG GCC GAC ATC CAG GAG TTT CCA GAT CTC AAA GGC ACC ACC AGC CTG GAG   100
                                                                                         300

      I   L   T   L   T   R   A   G   I   R   L   L   P   S   G   M   C   Q   Q   L
      ATC CTG ACC CTG ACC CGC GCA GGC ATC CGG CTG CTC CCA TCG GGG ATG TGC CAA CAG CTG   120
                                                                                         360

      P   R   L   R   V   L   E   L   S   H   N   Q   I   E   E   L   P   S   L   H
      CCC AGG CTC CGA GTC CTG GAA CTG TCT CAC AAT CAA ATT GAG GAG CTG CCC AGC CTG CAC   140
                                                                                         420

      R   C   Q   K   L   E   E   I   G   L   Q   H   N   R   I   W   E   I   G   A
      AGG TGT CAG AAA TTG GAG GAA ATC GGC CTC CAA CAC AAC CGC ATC TGG GAA ATT GGA GCT   160
                                                                                         480

      D   T   F   S   Q   L   Q   S   L   Q   A   L   D   L   S   W   N   A   I   R
      GAC ACC TTC AGC CAG CTG CAG TCC CTG CAA GCC CTG GAT CTT AGC TGG AAC GCC ATC CGG   180
                                                                                         540
```

FIG.8B

```
S   I   H   P   E   A   F   S   T   L   H   S   L   V   K   L   D   L   T   D
TCC ATC CAC CCT GAG GCC TTC TCC ACC CTG CAC TCC CTG GTC AAG CTG GAC CTG ACA GAC    200
                                                                                   600

N   Q   L   T   T   L   P   Q   L   A   G   L   G   L   M   H   L   K   L   K
AAC CAG CTG ACC ACA CTG CCC CAG CTG GCT GGA CTT GGG TTG ATG CAT CTG AAG CTC AAA    220
                                                                                   660

G   N   L   H   E   A   R   Q   E   A   E   Y   S   F   P   K   L   R   I   L
GGG AAC CTT CAC GAG GCA AGA CAA GAA GCT GAA TAT AGT TTC CCA AAA CTG AGG ATC CTG    240
                                                                                   720

E   V   P   Y   P   Y   A   R   S   D   W   D   M   C   A   S   F   F   K   A
GAG GTG CCT TAT CCT TAT GCC AGA TCA GAC TGG GAT ATG TGT GCC AGC TTC TTC AAG GCC    260
                                                                                   780

S   G   Q   A   A   E   W   S   K   P   K   Y   D   E   E   S   S   K   R   P
TCT GGC CAG GCT GCT GAG TGG TCA AAG CCA AAG TAT GAT GAG GAG TCT TCA AAA AGG CCC    280
                                                                                   840

L   G   L   L   L   L   L   D   L   L   L   Q   D   Q   D   L   D   E   L   Q
CTG GGC CTC CTT CTT CTT CTT GAT CTT CTC CTT CAG GAC CAG GAC CTG GAT GAG CTC CAG    300
                                                                                   900

L   E   M   E   M   E   D   M   E   E   L   V   Q   C   S   P   T   P   G   P
CTG GAG ATG GAG ATG GAG GAC ATG GAG GAG CTG GTC CAG TGT AGC CCT ACT CCA GGC CCC    320
                                                                                   960

F   K   P   Y   E   C   P   L   V   S   C   L   I   R   L   A   V   W   A   I
TTC AAG CCC TAC GAG TGT CCC CTC GTG TCC TGT CTG ATC CGC CTG GCC GTG TGG GCC ATC    340
                                                                                  1020

V   L   L   C   V   S   N   G   L   V   L   L   L   T   V   F   A   G   G   P
GTG TTG CTC TGC GTG TCC AAT GGA CTG GTG CTC CTG CTG ACC GTG TTC GCT GGC GGG CCT    360
                                                                                  1080
```

FIG. 8C

```
      A   L   P   P   V   K   F   V   G   A   I   A   G   A   N   T   L   T      380
GCC CTG CCC CCG GTC AAG TTT GTA GGT GCG ATT GCA GGC GCC AAC ACC TTG ACT      1140

      G   S   C   G   L   L   A   S   V   D   L   T   F   G   Q   F   S   E      400
GGC TCC TGT GGC CTT CTA GCC TCA GTC GAT CTG ACC TTT GGT CAG TTC TCT GAG      1200

      Y   A   R   W   E   T   G   L   G   C   A   T   G   F   L   A   V   L      420
TAC GCC CGC TGG GAG ACG GGG CTA GGC TGC GCC ACT GGC TTC CTG GCA GTA CTT      1260

      G   E   A   S   V   L   L   L   T   L   A   V   Q   C   S   V   S   V      440
GGG GAG GCA TCG GTG CTG CTG CTC ACT CTG GCA GTG CAG TGC AGC GTC TCC GTC      1320

      S   V   R   A   Y   G   K   P   S   L   G   S   V   R   A   G   V   L      460
TCC GTC CGG GCC TAT GGG AAG CCC TCC CTG GGC AGC GTT CGA GCA GGG GTC CTA      1380

      G   L   A   L   A   G   L   A   A   L   P   L   A   S   V   G   E   Y      480
GGC CTG GCA CTG GCA GGG CTG GCC GCA CTG CCC CTG GCC TCA GTG GGA GAA TAC      1440

      G   S   P   L   C   L   P   Y   A   P   E   G   Q   P   P   A   L   G      500
GGG TCC CCA CTC TGC CTG CCC TAC GCG CCT GAG GGT CAG CCA CCA GCC CTG GGC      1500

      F   V   A   L   V   M   M   N   S   C   F   L   A   V   V   G   A   Y      520
TTC GTG GCC CTG GTG ATG ATG AAC TCC TGT TTC CTG GCC GTC GTG GGT GCC TAC      1560

      I   L   Y   C   D   L   P   R   G   D   A   E   A   W   D   C   A   M      540
ATC CTG TAC TGT GAC CTG CCG CGG GGC GAC GCA GAG GCC TGG GAC TGC GCC ATG      1620
```

FIG. 8D

```
V   R   H   V   A   W   L   I   F   A   D   G   L   L   Y   C   P   V   A   F        560
GTG AGG CAC GTG GCC TGG CTC ATC TTC GCA GAC GGG CTC CTC TAC TGT CCC GTG GCC TTC    1680

L   S   F   A   S   M   L   G   L   F   L   P   T   V   V   K   S   V                580
CTC AGC TTC GCC TCC ATG CTG GGC CTC CTC TTC CCT ACG GTC CCC AAG TCT GTC            1740

L   L   V   V   L   P   A   C   L   N   P   L   L   Y   L   L   F   N                600
CTG CTG GTG GTG CTG CCT GCC TGC CTC AAC CCA CTG TAC CTG CTC TTC AAC                1800

P   H   F   R   D   D   L   R   R   L   R   P   P   A   G   P   G   P   L            620
CCC CAC TTC CGG GAT GAC CTT CGG CGG CTT CGG CCC GCA GGG CCC GGG CCC CTA            1860

A   Y   A   A   G   E   L   I   F   K   S   S   C   S   D   T   Q   A   L   V        640
GCC TAT GCT GCG GGG GAG CTG ATT AAG AGC TCC TGT GAT ACC CAG GCC CTG GTA            1920

A   F   S   D   V   D   L   I   L   E   A   S   E   E   A   G   R   P   G   L        660
GCC TTC TCT GAT GTG GAT CTC ATT CTG GAA GCT TCT GAA GGG CGG CCC GGG CTG            1980

E   T   Y   G   F   P   S   V   T   L   I   S   I   S   C   D   P   A   P   R        680
GAG ACC TAT GGC TTC CCC TCA GTG ACC CTC ATC TCC ATC TCC TGT CCA CCC AGG            2040

L   E   G   S   H   C   V   E   P   E   N   G   Q   H   F   G   N   P   Q   P   S    700
CTG GAG GGC AGC CAT TGT GTA GAG CCA GAG GGG AAC CAG TTT GGG AAC CCC CAA CCC TCC    2100

M   D   G   E   L   L   R   A   E   E   A   S   T   P   G   A   G   L   L   S        720
ATG GAT GGA GAA CTG CTG AGG GCA GAG GAG GGA TCT ACG CCA GCA GGT GGC TTG TCA        2160
```

FIG. 8E

```
 G   G   G   F   Q   P   S   G   L   A   F   A   S   H   V   *
GGG GGT GGC GGC TTT CAG CCC TCT GGC TTG GCC TTT GCT TCA CAC GTG TAA               737
                                                                                 2211

ATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCTCGGTGAATGATGGCTGCTTCTAAAACA   2290

AATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGCTCCAGCTTCACCTCTCTCCTGTGA   2369

CCATCACCAACGGGTGCCTCTTGGCCTTTCCCTTGGCCTTCTCAGCTTCACCTTGATACTGGGCCCTCTTCCTTG    2448

TCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGG  2527

TGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGTGATTTCCCGTGTGACTCATG   2606

GATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTT   2685

TGGAAGAGATTAAAAAAAAAAAAAAA                                                       2711
```
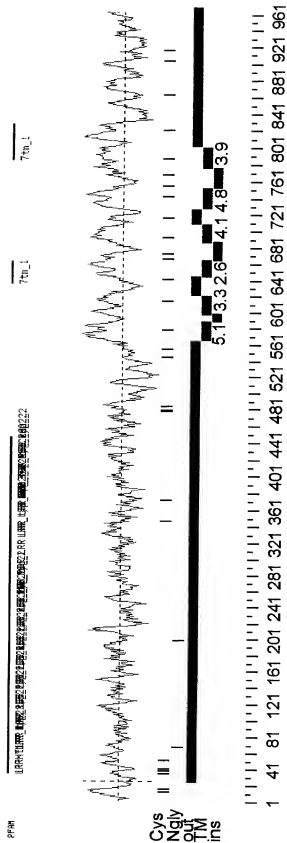
FIG. 9

FIG. 10A

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- -
HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq
- -

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR	Leucine Rich Repeat	241.4	1.3e-68	16
LRRNT	Leucine rich repeat N-terminal domain	27.2	0.00038	1
7tm_1	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
LRRNT	1/1	34	65	..	1	31	[]	27.2	0.00038
LRR	1/16	67	90	..	1	23	[]	12.4	11
LRR	2/16	91	114	..	1	23	[]	24.2	0.0031
LRR	3/16	115	138	..	1	23	[]	19.9	0.062
LRR	4/16	139	162	..	1	23	[]	16.4	0.7
LRR	5/16	163	186	..	1	23	[]	27.5	0.00031
LRR	6/16	187	210	..	1	23	[]	12.1	13
LRR	7/16	211	234	..	1	23	[]	21.6	0.019
LRR	8/16	235	257	..	1	23	[]	18.2	0.2
LRR	9/16	258	281	..	1	23	[]	19.0	0.11
LRR	10/16	282	305	..	1	23	[]	10.2	32
LRR	11/16	306	328	..	1	23	[]	5.6	1.5e+02
LRR	12/16	329	352	..	1	23	[]	8.8	52
LRR	13/16	353	374	..	1	23	[]	19.2	0.097
LRR	14/16	375	398	..	1	23	[]	16.9	0.49
LRR	15/16	399	422	..	1	23	[]	23.7	0.0042
LRR	16/16	423	446	..	1	23	[]	16.4	0.66
7tm_1	1/2	635	662	..	51	79	..	3.4	2.2
7tm_1	2/2	784	827	..	207	259	.]	1.1	11

FIG. 10B

Alignments of top-scoring domains:
LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038
```
        *->aCpreCtCsp..fglvVdCsgrgLtlevPrdlP<-*
          aCp++C+C +++  l+ dCs++gL +vP dl
  15088   34   ACPAPCHCQEdgIMLSADCSELGLS-AVPGDLD   65
```

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11
```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
           +LdLs N+Lt+l pglf++L+
  15088   67   LTAYLDLSMNnLTELQPGLFHHLR   90
```

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031
```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
           LeeL+Ls+N+L+++p +fs+L
  15088   91   FLEELRLSGNhLSHIPGQAFSGLY   114
```

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062
```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
           +L+ L L+nN+L ++p +++ Lp
  15088   115   SLKILMLQNNqLGGIPAEALWELP   138
```

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7
```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
           +L++L+L+ N ++ +p+ +f++L+
  15088   139   SLQSLRLDANlISLVPERSFEGLS   162
```

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031
```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
           +L++L+L+N Lt++p +++nLp
  15088   163   SLRHLWLDDNaLTEIPVRALNNLP   186
```

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13
```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
           L+  L  N+++++p+ +f+nL+
  15088   187   ALQAMTLALNrISHIPDYAFQNLT   210
```

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019
```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
           +L +L+L+nN+++l ++f++L
  15088   211   SLVVLHLHNNrIQHLGTHSFEGLH   234
```

FIG. 10C

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2
```
        *->nLeeLdLsnN.Ltslppglfsnlp<-*
          nLe+LdL++N+L+++p +++ L
15088  235   NLETLDLNYNkLQEFPV-AIRTLG   257
```

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11
```
        *->nLeeLdLsnN.Ltslppglfsnlp<-*
          +L+eL ++nN+++ +p+++f + p
15088  258   RLQELGFHNNnlKAIPEKAFMGNP   281
```

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32
```
        *->nLeeLdLsnN.Ltslppglfsnlp<-*
           L+++++ +N+++ + ++f+ Lp
15088  282   LLQTIHFYDNpIQFVGRSAFQYLP   305
```

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02
```
        *->nLeeLdLsnN..Ltslppglfsnlp<-*
          +L++L+L++ +++++p+ +++ +
15088  306   KLHTLSLNGAmdlQEFPD--LKGTT   328
```

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52
```
        *->nLeeLdLsnN.Ltslppglfsnlp<-*
          +Le L L + +++ lp+g +++Lp
15088  329   SLEILTLTRAgIRLLPSGMCQQLP   352
```

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097
```
        *->nLeeLdLsnN.Ltslppglfsnlp<-*
          +L++L Ls+N++++lp+ ++ ++
15088  353   RLRVLELSHNqlEELPS--LHRCQ   374
```

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49
```
        *->nLeeLdLsnN.Ltslppglfsnlp<-*
          +Lee+ L++N++ ++ ++fs+L+
15088  375   KLEEIGLQHNrlWEIGADTFSQLS   398
```

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042
```
        *->nLeeLdLsnN.Ltslppglfsnlp<-*
          +L+ LdLs N ++s++p++fs L
15088  399   SLQALDLSWNalRSIHPEAFSTLH   422
```

FIG. 10D

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66

```
        *->nLeeLdLsnN.LtslppglfsnLp<-*
          +L +LdL +N+Lt+lp   + +L
  15088   423   SLVKLDLTDNqLTTLPLAGLGGLM   446
```

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2

```
        *->dWpfGsalCklvtaldvvnmyaSillLta<-*
          +W  G ++C+ +++l v+ + aS+llLt+
  15088   635   RWETG-LGCRATGFLAVLGSEASVLLLTL   662
```

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11

```
        *->lCWlPyfivllldtlc.lsiimsstCelervlptallvtlwLayvNs
          l+  P + + +  +l ++      ++++++++v l++ + +
  15088   784   LLYCPVAFLSFASMLGlFPV----------
TPEAVKSVLLVVLPLPA 820
```

```
          clNPilY<-*
          clNP++Y
  15088   821 CLNPLLY   827
```

FIG. 11A

Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).

- -
HMM file: /ddm/robison/smart/smart/smart.all.hmms
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq
- -

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrntl		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
lrrntl	1/1	34	70	..	1	38	[]	25.7	0.0011
LRR_PS_2	1/13	64	87	..	1	24	[]	1.9	1.2e+02
LRR_typ_2	1/14	64	88	..	1	24	[]	12.6	2.1

FIG. 11B

LRR_bac_2	1/7	89	108	..	1	20	[]	0.9	80
LRR_PS_2	2/13	89	111	..	1	24	[]	17.2	0.4
LRR_typ_2	2/14	89	112	..	1	24	[]	32.1	1.3e-05
LRR_RI_2	1/4	89	115	..	1	28	[]	3.6	14
LRR_bac_2	2/7	113	132	..	1	20	[]	1.6	66
LRR_PS_2	3/13	113	136	..	1	24	[]	1.1	1.5e+02
LRR_typ_2	3/14	113	136	..	1	24	[]	19.2	0.1
LRR_bac_2	3/7	137	156	..	1	20	[]	0.1	1e+02
LRR_PS_2	4/13	137	159	..	1	24	[]	7.1	24
LRR_typ_2	4/14	137	160	..	1	24	[]	25.9	0.00095
LRR_PS_2	5/13	161	183	..	1	24	[]	11.4	6.6
LRR_typ_2	5/14	161	184	..	1	24	[]	27.5	0.00031
LRR_sd22_2	1/5	161	187	..	1	22	[]	5.3	31
LRR_RI_2	2/4	161	190	..	1	28	[]	5.3	8
LRR_PS_2	6/13	185	207	..	1	24	[]	7.0	25
LRR_typ_2	6/14	185	208	..	1	24	[]	23.2	0.0062
LRR_PS_2	7/13	209	232	..	1	24	[]	3.1	79
LRR_typ_2	7/14	209	232	..	1	24	[]	28.1	0.0002
LRR_RI_2	3/4	209	235	..	1	28	[]	1.2	31
LRR_sd22_2	2/5	233	235	..	1	22	[]	13.5	3
LRR_bac_2	4/7	233	252	..	1	20	[]	10.7	4.1
LRR_typ_2	8/14	233	255	..	1	24	[]	16.1	0.76
LRR_PS_2	8/13	233	255	..	1	24	[]	17.1	0.43
LRR_bac_2	5/7	256	275	..	1	20	[]	0.2	1e+02
LRR_PS_2	9/13	256	278	..	1	24	[]	2.9	85
LRR_typ_2	9/14	256	279	..	1	24	[]	24.4	0.0026

FIG. 11C

```
LRR_typ_2    10/14   327  350 . .   1   24 []    3.1     29
LRR_bac_2     6/7    351  370 . .   1   20 []   14.6    1.3
LRR_PS_2     10/13   351  372 . .   1   24 []   10.8      8
LRR_sd22_2    3/5    351  372 . .   1   22 []    7.6     16
LRR_typ_2    11/14   351  373 . .   1   24 []   18.8    0.13
LRR_RI_2      4/4    351  378 . .   1   28 []    2.6     19
LRR_PS_2     11/13   373  396 . .   1   24 []    2.3   1e+02
LRR_typ_2    12/14   374  396 . .   1   24 []    6.8     10
LRR_sd22_2    4/5    397  418 . .   1   22 []    7.0     19
LRR_PS_2     12/13   397  419 . .   1   24 []   13.6    3.4
LRR_typ_2    13/14   397  420 . .   1   24 []   30.4  4.3e-05
LRR_bac_2     7/7    421  440 . .   1   20 []    5.8     18
LRR_sd22_2    5/5    421  441 . .   1   22 []    3.7     49
LRR_PS_2     13/13   421  442 . .   1   24 []    5.5     39
LRR_typ_2    14/14   421  444 . .   1   24 []   21.6   0.018
```

Alignments of top-scoring domains:
lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011

```
              *->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-*
                 +CPapC+C ++    ++ dCs++gL    +vP dl + t +
 15088    34     ACPAPCHCQEdGIMLSADCSEIGLS--AVPGDLDPLTAY      70
```

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02

```
              *->LtsL.qvLdLsnNnLsGeIPssLgn<-*
                 L  L+ +LdLs NnL+ e+ + l+
 15088    64     LDPLtAYLDLSMNNLT-ELQPGLFH         87
```

FIG. 11D

```
LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
                   *->lpnL.reLdlsnNqltsLPpgaFgg<-*
                     L  L+  LdlS N+Lt+L pg+F++
        15088   64   LDPLtAYlDLSMNNLTElQPGlFHH                88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
                   *->PpsLkeLnvsnNrLteLPeL<-*
                     +L+eL+ s+N+L+  P
        15088   89   LRFlELRLSGNHLSHIPGQ                108

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
                   *->LtsLqvLdlsnNnLsGeIPsslgn<-*
                     L+ L++L+Ls+N+Ls +IP + ++
        15088   89   LRFlELRLSGNHLS-HIPGQAFS                111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
                   *->lpnLreldlsnNqltsLPpgaFgg<-*
                     L+ L+eL+Ls+N+L+++P +aF+g
        15088   89   LRFlELRLSGNHLSHIPGQAFSG                112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
                   *->npsLreLdlsnNkl.gdeGaraLaeaLks<-*
                     ++ L+eL+Ls+N+l+++ G  +  ++L s
        15088   89   LRFlELRLSGNHLsHIPG--QAFSGlYS              115
```

FIG. 11E

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
```
              *->PpsLkeLnvsnNrlteLPeL<-*
                 sLk+L   +nN+L   P+
   15088    113  LYSLKIMLQNNQLGGIPAE      132
```

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
```
              *->ItsLqvIdIsnNnLsGeIPssIgn<-*
                 L sI++L L+nN+L G   + l+
   15088    113  LYSLKIMLQNNQLGGIPAEALWE      136
```

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
```
              *->IpnLreIdIsnNqLtsLPpgaFgg<-*
                 L +L+ L L+nNqL  +P+ta++
   15088    113  LYSLKIMLQNNQLGGIPAEALWE      136
```

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
```
              *->PpsLkeLnvsnNrlteLPeL<-*
                 psL++l+ + N ++ Pe
   15088    137  LPSLQSLRLDANLISLVPER      156
```

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
```
              *->ItsLqvIdIsnNnLsGeIPssIgn<-*
                 L+sLq+L+L N +s  +P+ +
   15088    137  LPSLQSLRLDANLIS-LVPERSFE      159
```

FIG. 11F

```
LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
                  *->LpnLreIdLsnNqLtsLPpgaFgg<-*
                     Lp+L++L+L+ N ++ +P++ F+g
15088    137         IPSLQSIRLDANLISLVPERSFEG       160


LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
                  *->LtsLqvIdLsnNnLsGeIPsslgn<-*
                     L+sL++L L +N L+ eIP        n
15088    161         LSSLRHLWLDDNALT-EIPVRALN      183


LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
                  *->LpnLreIdLsnNqLtsLPpgaFgg<-*
                     L++Lr+L L++N+Lt++P +a+++
15088    161         LSSLRHLWLDDNALTEIPVRALNN      184


LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
                  *->LtnLeeIdLsqNkI.....kkiENLde<-*
                     L+ L++L+L +N +++ + + + NL
15088    161         LSSLRHLWLDDNALteipvRALNNLPA      187


LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
                  *->npsLreIdLsnNkLgdeGaraL..aeaLks<-*
                     ++sLr L+L +N l++ +raL++  aL++
15088    161         LSSLRHLWLDDNALTEIPVRALnnLPALQA      190
```

FIG. 11G

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25

```
              *->ltsLqvldlsnNnlsGeIPsslgn<-*
              L+ Lq   L+ N++s  +IP+    ++
15088   185   LPALQAMTLAlNRIS-HIPDYAFQ        207
```

LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062

```
              *->lpnLreldlsnNqltsLPpgaFqg<-*
              Lp+L+    L   N++++P+ aFq+
15088   185   LPALQAMTLAlNRISHIPDYAFQN        208
```

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79

```
              *->ltsLqvldlsnNnlsGeIPsslgn<-*
              ltsI+vL+l+nN++       s+
15088   209   LTSLVVLHLHNNRIQHLGTHSFEG        232
```

LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002

```
              *->lpnLreldlsnNqltsLPpgaFqg<-*
              L++L +L+l+nN+++L     F+g
15088   209   LTSLVVLHLHNNRIQHLGTHSFEG        232
```

LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31

```
              *->npsLreldlsnNkldeGaraLaeaLks<-*
              ++sL +L+L nN +   G   + e+L+
15088   209   LTSLVVLHLHNNRIQHLGTHSF-EGLHN       235
```

FIG. 11H

```
LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5,  E = 3
                    *->LtnLeeLdLsqNkI....kkiENLde<-*
                      Lt L++L L +N+I++ +++++E+L++
            15088  209  LTSLVVLHLHNNRIqhlgtHSFEGLHN       235

LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7,  E = 4.1
                    *->PpsLkeLnvsnNrLteLPeL<-*
                      ++L+++L+ ++N+L e+P
            15088  233  LHNLETLDLNYNKLQEFPVA       252

LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1,  E = 0.76
                    *->IpnLreLdLsnNqLtsLPpgaFgg<-*
                      L+nL++LdL++N+L++ P + +
            15088  233  LHNLETLDLNYNKLQEFPVAI-RT       255

LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1,  E = 0.43
                    *->LtsLqvLdLsnNnLsGeIPssIgn<-*
                      L++L++LdL++N+L e+P +
            15088  233  LHNLETLDLNYNKLQ-EFPVAIRT       255

LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2,  E = 1e+02
                    *->PpsLkeLnvsnNrLteLPeL<-*
                      +L+eL+ nN+++ Pe
            15088  256  LGRLQELGFHNNNIKAIPEK       275
```

FIG. 11I

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85

```
           *->LtsLqvLdLsnNnLsGeIPsslgn<-*
              L +Lq+L ++nNn+   IP+ +
15088   256   LGRLQELGFHNNNIK-AIPEKAFM        278
```

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026

```
           *->LpnLreldLsnNqLtsLPpgaFqg<-*
              L+ L+eL   +nN++++P+ aF g
15088   256   LGRLQELGFHNNNIKAIPEKAFMG        279
```

LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29

```
           *->LpnLreldLsnNqLtsLPpgaFqg<-*
              ++L+ L L +  ++ LP+g++q
15088   327   TTSLELTLTRAGIRLLPSGMCQQ         350
```

LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3

```
           *->PpsLkeLnvsnNrLteLPeL<-*
              p+L+ L s+N++eLP L
15088   351   LPRLRVLELSHNQIELPSL             370
```

LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8

```
           *->LtsLqvLdLsnNnLsGeIPsslgn<-*
              L++L+vL+Ls+N++  e+Ps l +
15088   351   LPRLRVLELSHNQIE-ELPS-LHR        372
```

FIG. 11J

```
LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
                *->ltnLeeldlsqNkikiENlde<-*
                   L +L++L+Ls+N+I+  L+
15088   351     LPRLRVLELSHNQIEEIPSLHR      372


LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
                *->LpnLreLdlsnNqLtsLPpgaFgg<-*
                   Lp Lr+L Ls+Nq+++LP + ++
15088   351     LPRLRVLELSHNQIEELP-SLHRC       373


LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
                *->npsLreLdlsnNklgdeGaraLaeaLks<-*
                   +p+Lr+L Ls+N + +   + ++ L++
15088   351     LPRLRVLELSHNQIEELPSLHRCQKLEE       378


LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
                *->LtsLgvLdLsnNnLsGeIPsslgn<-*
                   +++L+++ L++N++   +++++
15088   373     CQKLEIGLQHNRIWEIGADTFSQ       396


LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
                *->LpnLreLdlsnNqLtsLPpgaFgg<-*
                   +L+e  L++N++ ++ +++F+
15088   374     -QKLEIGLQHNRIWEIGADTFSQ       396
```

FIG. 11K

LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19

```
          *->LtnLeeLdLsqNkIkkiENLde<-*
            L+ L+ LdLs+N I++i
15088  397  LSSLQALDLSWNAIRSIHPEAF      418
```

LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4

```
          *->LtsLqvLdLsnNnLsGeIPsslgn<-*
            L+sLq LdLs+N +  +I ++ ++
15088  397  LSSLQALDLSWNAIR-SIHPEAFS      419
```

LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05

```
          *->LpnLreLdLsnNqLtsLPpgaFqg<-*
            L++L+ LdLs+N+++s++p+aF+
15088  397  LSSLQALDLSWNAIRSIHPEAFST      420
```

LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18

```
          *->PpsIkeLnvsnNrIteLPeL<-*
            +sL +L+  +N+Lt+LP
15088  421  LHSLVKLDLTDNQLTTLPLA      440
```

LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49

```
          *->LtnLeeLdLsqNkIkkiENLde<-*
            L+ L+ LdL +N+++ +  L +
15088  421  LHSLVKLDLTDNQLTTL-PLAG      441
```

FIG. 11L

```
LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
              *->LtsLqvldlsnNnlsGeIPsslgn<-*
                 L+sL+ LdL +N+L+ ++P    g
15088   421      LHSLVKLDLTDNQLT-TLPL-AGL      442


LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
              *->LpnLreLdlsnNqLtsLPpgaFqg<-*
                 L++L +LdL +NqLt+LP  ++g
15088   421      LHSLVKLDLTDNQLTTLPLAGLGG      444

//
```

FIG.12A

GAP of: FrGcgManager_101_HTAUB3ha_   check: 2817   from: 1   to: 3637

mLGR6 - 1 (analysis only) - Import - complete

to: FrGcgManager_101_ITA0flsO_   check: 3059   from: 1   to: 2711

corrected human LGR6 (analysis o - Import - complete

Symbol comparison table:
/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight:	12	Average Match:	10.000
Length Weight:	4	Average Mismatch:	0.000

Quality:	21826	Length:	3688
Ratio:	8.051	Gaps:	20
Percent Similarity:	84.248	Percent Identity:	84.211

Match display thresholds for the alignment(s):

```
        | = IDENTITY
        : = 5
        . = 1
```

FIG. 12B

FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLsO_

```
901  CCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAACTAT  950
                  ||||||||||||||||||||||||||||||||  ||
   1  ..........GGGCTGCACAATCTGGAGACACTAGACCTGAATTAT   36

951  AATGAGCTGCAGGAGTTCCCCTGGCTATCCGGACCCCTGGGCAGACTGCA  1000
     ||  ||||||||||||||     ||||  ||||||||||||||||||||||
  37  AACAAGCTGCAGGAGTTCCCCTGGCCATCCGGACCCCTGGGCAGACTGCA   86

1001 AGAATTGGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT  1050
      |||  |||| ||||||||||||||||||||||||||  ||| |||
  87  GGAACTGGGGTTTCCATAACAACAACATCAAGGCCATCCCAGAAAAGGCCT  136

1051 TCATGGGCAACCCCTCTCCTGCAGACAATACATTTTTATGACAACCCAATC  1100
     ||||||| ||| |||| |||||||| |||||||| |||||||||||||||||
 137 TCATGGGGAACCCCTCTGCTACAGACGATACACTTTTTATGATAACCCAATC  186

1101 CAGTTTGTGGGAAGGTCAGCATTCCAGTACCTGTCTAAACTGCATACCGCT  1150
     ||||||||||||| || | ||||| ||||||||||||| |||||| || ||
 187 CAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT   236
```

```
1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCCCAGACCTCAAAGGCA 1200
     |||| ||||||||| ||  ||||  |||| ||||  |||||  ||||||||||
 237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA  286

1201 CCACTAGCCTGGAGATCCTGACCTGACCCGTGCGGGCATCAGACTGCTC 1250
     ||||  |||||||||||||  |||||||  | |||||||  |||||||||||
 287 CCACCAGCCTGGAGATCCTGACCCTGACCCGTGCGGGCATCCGGCTGCTC  336

1251 CCACCGGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC 1300
     |||  |||  ||||||||||||||||||||  ||||||  |||||| |||||
 337 CCATCGGGGATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAACTGTC  386

1301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCGACAGATGTCAGAAGCTGG 1350
     ||| |||| || ||||| |  |||||||||||  |  ||||||  ||||||
 387 TCACAATCAAAATTGAGGAGCTGCCCAGCCTGCGACAGGTGTCAGAAATTGG  436

1351 AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
     ||||||| |||||  |||   |||||||| |||  |||||||  ||  ||||
 437 AGGAAATCGGCCTCCAACACAACCACCGCATCTGGGAAATTGGAGCTGACACC  486

1401 TTCAGCCAGCTGGGCTTCCTTGCAAGCTTTAGACCTGAGTTGGAAATGCCAT 1450
     |||||||||||  ||||||| ||||||||  |||||  || ||||||||||||
 487 TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGGATCTTAGCTGGAACGCCAT  536

1451 CCGTGCCATCCACCCTGAGGCTTTTCTCAACCCTTCGATCCTTGGTTAAGC 1500
     ||| |||||||||||  || |||||||| |||||  || | ||||| |||||
 537 CCGGTCCATCCACCCCTGAGGGCCTTCTCCACCCTGCACTCCCCTGGTCAAGC  586
```

FIG. 12D

```
1501  TGGACCTGACTGACAACCAGCTGACCACACTGCCCCTGGCTGGCTGGGA  1550
      ||||||||| |||||||||| |||||||||||||||||||||| || ||
587   TGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGCTGGACTTGGG  636

1551  GGCCTGATGCACCTGAAGCTCAAAGGGAACTTGGCCCTGTCTCAGGCCTT  1600
      ||| ||||||| ||||||||||||||| | || |||| |||||||||||
637   GGCTTGATGCATCTGAGGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCTT  686

1601  CTCCAAGGACAGTTTCCCAAAAACTGAGGATCCTGGAGGTGCCCTACGCCT  1650
      ||||||||||||||||||||||||||||||||||||||| || ||||
687   CTCCAAGGACAGTTTCCCAAAAACTGAGGATCCTGGAGGTGCCCTATGCCT  736

1651  ACCAGTGCTGTGCCTACGGCATCTGTGCCAGCTTCTTCAAGACCCTCTGGG  1700
      |||||||||| |||| | ||  | |||||||||||||||| |||||||
737   ACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG  786

1701  CAGTGGGCAGGCCCGAGGACTTTCATCCAGAAGAGAGGAGGCACCAAAGAG  1750
      |||||| |||| || |  |  ||| | || |||| |||| |
787   CAGTGGGAGGCGTGAAGACCTTCACCTTGATGATGAGGAGGTCTTCAAAAAG  836

1751  GCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCACTATGACCTAGACC  1800
      |||||||| |||||| |||| ||||||| |||||| ||| ||
837   GCCCCTGGGCCTCCTTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACC  886

1801  TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCCAGTGTC  1850
      |||||||||||||||| ||| |  |||||||| ||||||
887   TGGATGAGCTCCAGCTGGACGATGAGGAGGACTCAAAGCCACACCCCAGTGTC  936
```

FIG. 12E

```
1851 CAGTGCAGCCCTGTTCCAGGCCCCTTCAAGCCCTGCCGAGCACCTCTTTGA 1900
     ||||| |||||| ||||||||||||||| ||| |||||||||||
937  CAGTGTAGCCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGA  986

1901 GAGCTGGGGCATCCGCCTTGCTGTGTGGGCCATCGTGCTGCTCCCGTAC 1950
     |||||||||||||| || ||||||||||||| ||||||||| ||||||
987  AAGCTGGGGCATCCGCCTGGCCGTGGGCCATCGTGTTGCTCTCCCGTGC 1036

1951 TCTGTAACGGGCTGGTGCTGCTGACAGTCTTTGCCAGCCGGACCCAGCCCG 2000
     |||| || || ||||||||||||| || || ||| |||       |||
1037 TCTGCAATGGACTGGTGCTGCTGACCGTGTTCCGCTGGCCGGCCTGCCCCC 1086

2001 CTGTCCCCGTCAAGCTTGTGGTGCGGATGGCAGGCGCCAACGCCCT 2050
     ||| |||| ||||| ||||| |||| |||| |||||||||| || ||
1087 CTGCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAACACCTT 1136

2051 GACGGGGCAATTTCCTGTGGTCTCCTGGCCCTCTGTGGACGCCTTGACCTATG 2100
     || |||||||| ||  || || ||| ||||||| |||| |||||||
1137 GACTGGCATTTCCTGTGGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTG 1186

2101 GTCAGTTCGCTGAGTATGAGCCCCTGGGGAGAGCGGGTCTGGGCTGCCAG 2150
     ||||||||| ||||| |||||||||||||||| |||| ||| |||||
1187 GTCAGTTCTCTGAGTACGAGCCCCGGGGAGAGACGGGCTAGGCTGCCGG 1236

2151 GCTACGGGCTTCCTGGCTGTCCTGGTTCAGAGAGGCGTCGGTGCTGCTGCT 2200
     || || ||||||||| || ||  || |||| ||||| |||||||||||||
1237 GCCACTGGCTTCCTGGCAGTACTTGGGTCGGAGGCCATCGGTGCTGCTGCT 1286
```

FIG. 12F

```
2201  CACACTGGCGGGCCGTGCAGTGCAGCAGCATCTGTGACCTGCGTCCGAGCCT  2250
      ||| ||||||  ||  |||||||||| |||| ||  |||| ||||| ||||
1287  CACTCTGGCCCCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGGCCT  1336

2251  ACGGGAAGGCGCCGTCGCCTGGCAGCGTCCGCGCAGGCCGCCACTGGGATGC  2300
      | |||||  | || || |  ||||||| || ||||  || |  || || |||
1337  ATGGGAAGTCCCCCTCCCTCGGGCAGCGTTCGAGCAGGGGTCCTAGGCTGC  1386

2301  CTGGCGCTGGCCGGGCTGGCCGCAGCACTGCCCGCTGGCCTCGGTGGGAGA  2350
      |||| |||||  |||||||  |||||||| ||||||||| || |||||||||
1387  CTGGCACTGGCAGGGCTGGCCGCGCCCACTGCCCCTGGCCTCAGTGGGAGA  1436

2351  GTATGGCGCCTCCCCACTCTGCCCTGCCCTACGCGCCCCACCCGAGGGCCGGC  2400
      || || ||||||  ||||| |||||||  ||||| ||||| ||| |||
1437  ATACGGGGCCCTCCCCACTCTGCCCTCCCCTACGCGCCACCTGAGGGTCAGC  1486

2401  CGGCCGCCCCTGGGCTTCGCTGTAGCCCTGTGATGAATGAACTCGCTCTGC  2450
      | || |||||||||| | ||  ||||||||| |||||||||||||||  |||
1487  CAGCAGCCCTGGGCTTCACCGTGGCCCTGTGATGATGAATGAACTCCTTCTGT  1536

2451  TTCCTGGTGGTGGCCGGCGGCCCTACATCAAGCTCTACTGTGACCTGCCACG  2500
      |||||||| ||||||| ||||||||| || | |||||||| |||||||
1537  TTCCTGGTCGTGGCCGGGTGCCTACATCAAACTGTACTGTGACCTGCCGCG  1586

2501  GGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGCGCCACGTGGCCT  2550
      ||| |||||||||||||||||||||||| | ||||||||||||||||||
1587  GGGCGACTTTGAGGCCGTGTGGGACTGCGCGCCATGGTGGAGGCCACGTGGCCT  1636
```

FIG. 12G

```
2551 GGCTCATCTTTGCAGAGATGGCCTCCTCCTTACTGCCCCGTGGCCTTCCTCAGC 2600
     |||||||||| ||||| || |||||||||| |||||||||||||||||||||||||
1637 GGCTCATCTTCGCAGACAGGGCTCCCTCTACTGTCCCGTGGCCTTCCTCAGC 1686

2601 TTTGCCTCCATGCTGGGCCTCTTCCCTGTCACCCCCGAGGCTGTCAAGTC 2650
     || |||||||||||||||||||||||||||| ||||||| ||||||| |||
1687 TTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGTC 1736

2651 AGTCCTTCTGGGTGGTGCTGCCCTGCCTGCCTCAACCCACTGCTCT 2700
     ||||| ||||||||||||| ||||||||||||||||||||||| |
1737 TGTCCCTGCTGGTGGTGCTGCCCCTGCCTGCCTCAAACCCACTGCTGT 1786

2701 ACCTGCTCTTCAACCCTCACTTCCGGGATGACCTTCGGCGGCTCTGGCCA 2750
     ||||||||||||||||||||||||||||||||||||| ||||
1787 ACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGGCTTCGGCCC 1836

2751 AGCCCTCGGTCCCCAGGGCCCCTAGCCTACGCTGCTGCCGGTGAGCTGGA 2800
     || | |  | |||||||| ||||| ||||| ||||| ||||||||
1837 CGCGCAGGGACTCAGGGCCCCCTAGCCTATGCTGCGGGCCCGGGAGCTGGA 1886

2801 GAAGAGCTCCTGCGACTCCACCCAAGCGCTGGTGGCTTTCTCAGATGTGG 2850
     ||||||||||| || || ||||| || ||||| || ||||| || |||||
1887 GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTCTGATGTGG 1936

2851 ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGGCTAGAGACC 2900
     ||||| |||||||||||||| ||||||||| ||| |||||||| ||||||
1937 ATCTCATTCTGGAAGCTTCTGAAGCTGGGCGGCCGCCCCTGGGCTGGAGACC 1986
```

FIG. 12H

```
2901 TATGGCTTCCCTTCAGTGACCCTCATCTCCGACATCAGCCGGGGGCCAC 2950
     ||||||||| ||||||||||||||||| || |||| ||| ||||
1987 TATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCCAGCCAGGGGCCCC 2036

2951 CAGGCTGGAGGGAAACCATTTATAGAGTCTGATGGAACCAAGTTTGGGA 3000
     ||||||||||| | ||||| | ||||| || |||| || | ||||||
2037 CAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA 2086

3001 ACCCACAACCTCCCATGAAGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC 3050
     ||||| ||||| ||||| | |||||||||||||||| ||||||||| |
2087 ACCCCCAACCCTCCATGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT 2136

3051 ACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGGAGCCCCTCTGGCCCCTCTGG 3100
     || ||||| | |||| || | |||||||  | | |||||||||
2137 ACGCCAGCAGGTGGAGGCTTGTCAGGGGGTGGCGGCTTTCAGCCCCTCTGG 2186

3101 CTCTCTCTTTGCCTCCTCACTTGTAAATATCCCT.............. 3133
     ||    ||||| || ||||||||||||||||
2187 CTTGGCCCTTTGCTTCACACGTGTAAATATCCCTCCCCCATTCTTCTCTTCC 2236

3134 .CTCTGTT...TGTC...CTCTCCCCATC...CAATGATGGCTGCTTATAA 3174
     |||| || | | |||||||| ||  |||||||||||||||||||||
2237 CCTCTCTTCCCTTTCCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAA 2286

3175 AAGAAAGACAACTCCAAC...........TCCAATAGCAAGATGGCCAAC 3212
     || |||| ||||| || ||||||| |||||| |
2287 AACAAATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAG 2336
```

FIG. 12I

```
3213  ACCTCTGACTCCATTGTT.....CTCTCTCCACGACCCCTAACCAATGAGTG 3259
        | ||| ||||| || ||    |||||||      || |  ||||  | ||
2337  TAC.CTGGCTCCACTGATCACCCTCTCTCCCTGTGACCATCACCAACGGGGTG 2385

3260  CTTCCAAGTCTTGCTTGTCTTGGCCT...TCAGCTTCACTTTCACCCTG 3306
        | ||      |||| ||  |||  ||   |||||||||||  ||| |
2386  CCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTG 2435

3307  GGC..CTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCTGGGAAATT 3353
        |||    |||| |||| || || |  |  ||| | ||||| |||||
2436  GGCCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT 2485

3354  ...TGCATAGGAGAGAAAGGAGAAAAGACAAAAGACAGTGAAGGTTATTGGGC 3400
        |||  | |||| ||| ||  ||||||||||||||||||        |||
2486  GTCTGCTTAAGGGAAATGAGGGAAG.TAAAGACAGTGAAG......GGG. 2527

3401  CCTGACAGAGCCATGATCAGTAAGTGCAGAGT.GATGGGGAGGTCTCACA 3449
        || |   |||  || ||||  |||| |||| ||| || ||||| |||||
2528  ..TG...GAGGGTTGATC....AGGGCACAGTGGACAGGGAGACCTCACA 2568

3450  GAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTG 3499
        |||||   |  | ||||||  | | |          | | |
2569  GAGAAAGGC.CTGGAAGGTGATTTCC.........CGTGTGACTC.... 2603

3500  TGACATATAGAATATAAAATGTGTTCTGCGTTCCATTAATCTTGACCTAT 3549
        |  |  ||| ||| |  | ||| | ||  |||||||| |||||| |||
2604  ..ATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATAT 2651
```

FIG. 12J

```
3550 GCTGNGCCAAAGTGCTTCCTGTTAAAATACACTTTGGAAGACATTGAAAA 3599
          ||  :||  ||    ||||||  ||||||||   |||||||||||||  |||  ||||
2652 GCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATTAAAAA 2701

3600 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGCGGCCGC 3637
          ||||||||||
2702 AAAAAAAAA............................... 2711
```

FIG. 13A

GAP of: FrGcgManager_102_MTA0uXMaE check: 8470 from: 1 to: 968

mLGR6.aa (analysis only) - Import - complete

to: FrGcgManager_102_NTAf7nCl_ check: 5092 from: 1 to: 737

corrected hLGR6.aa (analysis onl - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248
Quality:	3424	Length:	968
Ratio:	4.646	Gaps:	0
Percent Similarity:	90.773	Percent Identity:	89.281

Match display thresholds for the alignment(s):

```
             | = IDENTITY
             : = 2
             . = 1
```

FIG. 13B

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nCl_ May 5, 19100 15:04

```
201 IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP 250
                      ||||||||||||||.||||
  1 ................GLHNLETLDLNYNKLQEFP  19

251 LAIRTLGRLQELGFHNNNIKAIPEKAFWMGNPLLQTIHFYDNPIQFVGRSA 300
    .|||||||||||||||||||||||||||||||||||||||||||||||||
 20 VAIRTLGRLQELGFHNNNIKAIPEKAFWMGNPLLQTIHFYDNPIQFVGRSA  69

301 FQYLSKLHTLSLNGATDIQEFPDLKGTSLEILTLTRAGIRLLPPGVCQQ 350
    ||||.||||||||||||.||||||||||||||||||||||||||..||
 70 FQYLPKLHTLSLNGAMDIQEFPDLKGTSLEILTLTRAGIRLLPSGMCQQ 119

351 LPRLRILELSHNQIEELLPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
    ||||:|||||||||||||||||||||||.||||| ||||||||| ||
120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169

401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
    ||||||||||| .|||||| |||||||||||||||||||||||||||||
170 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 219
```

FIG. 13C

```
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF   500
    |||||||||||||||||||||||||||| ||.|||| |||::|||
220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL   269

501 HPEEEEAPKRPLGLLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCCSPVPG   550
    | ::||.||||||| ||||||| |||||: |||||.||||||| |
270 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCCSPTPG   319

551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLV   600
    |||||||||||||||||||||||||||||||||||| ||.|| |||| |
320 PFKPCEXLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV   369

601 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV   650
    ||| |.||||.|||||||||||||.||:.|||.||||.||||.||||||
370 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV   419

651 LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLAIAGLA   700
    |||||||||||||||||||::|.:||||| |||||||||||||||||||
420 LGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVIGCLALAGLA   469

701 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFIVVAGA   750
    ||||||||||||||||||||||:|||| |||||| ||||||| ||||||
470 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA   519

751 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIIFADGLLYCPVAFLSFASMLGL   800
    |||||||||||||||||||||||||||||||||||||||||||||||||
520 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIIFADGLLYCPVAFLSFASMLGL   569
```

FIG. 13D

```
801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP 850
    ||||||||||||||||||||||||||||||||||||||||||| |   ||
570 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGP 619

851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 900
    ||||||||||||||||||||||||||||||||||||.||||||||||||
620 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 669

901 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS 950
    ||| ||| |||.| :| :|  ||||||  |  ||||||:|||:.| || |
670 LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL 719

951 SVGGALWPSGSLFASHL* 968
    | || ||| |||| |-|
720 SGGGGFQPSGLAFASHV* 737
```

FIG. 14A

>15088
> Fbh150881 - Import - vector trimmed

```
CGGCCGGCGGTGCAGCCCGCCGGGACCGGGAGGCGGAGCTGCGGCCACCGCGCCGTGCG
TCCGCGGCCGGCCGGCAGGTGCCCCAGTAGCCCGCCACCGCGCGAGATGCCCAGCCCGCGGGG
GCTCCGGGCGCTATGGCTTTGCCGCGGCGCTGTGCGCTTCCCGAGGGCCGGCGGCGCGCCCC
CCAGCCCGGCCCGGGCCCACCGCGCCTGCCCGCCCCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTCTGCCGACTGCTCTGAGCTCGGGCTGTCCGCCGTTCCGGGGGACCTGGACCC
CCTGACGGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGGCCTCTT
CCACCACCTGGCCTTCTTGGAGGAGCTGCGTCTCTTCTCTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTCTGTCTCTCTACAGCCTGAAAATCCTGAGTGCTGCAGAACAATCAGCT
GGGAGGAAATCCCGCAGAGGCCGCTGTGGGAGCTGCCAGACCCTGCAGTCGCTGCGCCTAGA
TGCCAACCTCATCTCCCTGGTCCCCGGAGAGAGCTTTGAGGGGCTGTCCTCCCTCCGCCCA
CCTCTGGCTGGACAAATGCACTCACGGAGATCCGTGTACAGAAGCCCTCAACAACCTCCC
TGCCCTGGCAGGCCATGACCCTGGCCCTCAACCGCATCAGCCACACATCCCCGACTACCGCGTT
CCAGAATCTCACCAGCCTTGTGGTGCTGCATTTGCATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGGCTGACAATCTGGACACTAGACCTGAATTATAAACAAGCT
GCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCAGGAACTGGGGTTCCATAA
CAACAACATCAAGGCCATCCCAGAAAAGCCTTCATGGGGAACCCCTCTGCTACAGACGAT
ACACTTTTATGATAACCCAATCCAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAA
ACTCCACACTATCTCTGAATGGTGCCATGGACCACCGCAGGCATCCGGCTGCTCCCATCGGG
CACCACCAGCCTGGAGATCCTGAGCTGCCCAGGCTCCGAGTCCTGGAACTGTCTCCAATCAAATTGAGGA
GATGTGCCAACAGCTGCCACAGGTGTCAGAAATTGGAGGAAAATCGGCCTCCAACAACCGCCAT
CTGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAAGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGGCTGGACTTGGGGCTTGAT
GCTGGACCTGACAGCAACAACCAGCTGACCACACTGCCCCCTGGCTGGACTTGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCTTCTCCCAAGGACAGTTTCCC
```

FIG. 14B

```
AAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGCTGTCCCTATGGGATGGTGTGC
CAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTTGAAGACCTTGATGATGAGGA
GTCTTCAAAAGGCCCCTGGGCCTCCTTGCCAGACAAGCAAGCAGAGAACCACTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAG
CCCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAAGCTGGGGCATCCGCCT
GGCCGTGGGGCCATCGTTGTTGCTCTCCCGGTCCAATGGACTGGTGCTGCTGACCGT
GTTCGCTGGCGGGCCTGCCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGG
CGCCAACACCTTGACTGGGCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT
TGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGACGGGGCTAGGCTGCGCCGGGCCACTGG
CTTCCTGGCAGTACTTGGTCGGAGGCATCGGTCGTGCTGCTCACTCTGGCCGCAGTGCA
GTGCAGGGGTCCTAGGCTGCCTGGCAGGGCTGGCGCCGCGCACTGCCCCTGGC
TCGAGCAGGGTCCTAGGCTGCCTGGCAGGGCTGCCCTACGCGCCACCTGAGGGTCA
CTCAGTGGGAGAATACGGGGCCCTCCCACTCTGGTGATGATGAACTCCTTCTGTTTCCTGGT
GCCAGCAGCCTGGGCTTCACCGTGGCCTTGGCCGGGGACCTTTGAGGCCGT
CGTGGCCGGTGCCTACATCAAACTGTACTGGACCTGCCCGGCGGGGGGACTTTGAGGCCGT
GTGGGACTGCCGCCATGGTGAGGCACGTGGCCCTCTTCCCGCCTCTTCCGTGTCACGCCCGA
CTGTCCCGTGGCCTTCCTCCAGCTTCGCTGGTGTCTGCCCCTGCCTGCCTCAACCCACTGCT
GGCCGTCAAGTCTGTCTGCTGGTGGTGTGCTGCCCCCGCCTTCGGCGCGGTTCGGCCCCGGCAGG
GTACTGCTCTTCAACCCCACTTCCGGATGACCTTCGGCGGCTGGAGAAGAGCTCCTGTGATTC
GGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGAGCTGGAAGCTTCTGAAGCTGG
TACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTGGAAGCCCTGACCCTGTCAGCA
GCGGCCCCCTGGGCGTGGAGGACCTATGGCTTCCCCTCAGTGACCGTGAGAGGGAACCACTTTGG
GCCAGGGCGCCCAGGCTGAGGGCAGCCATTGTGTAGAGCCAGAGGGATCTACGCCAGC
GAACCCCAACCTCCATGGATGGAGAACTGCTGCTGGAGGGCCTGCCTTTGCTTCACA
AGGTGGAGGCTTGTCAGGGGGTGGGCGGCTTTCAGCCCCTCTGCCCTCTTTCCCTTCCCTCTCCCCCTC
CGTGTAAAATATCCCTCCCATTCTTCTTCCCCTCTTCCCTTTCCCTCTCTCCTCCCCCTC
GGTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCTATAGC
```

FIG. 14C

AGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGT
GCCTCTTGGCCTGGCCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTC
CTTGTCATGTCTGAAGCTGTGGACCAARAGACCTGGACTTTTGTCTGCTTAAGGGAAATGA
GGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCT
CACARAAAAGGCCTGGAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAAATGTG
TTCCATGTACCATTAATCTTGACATATGCCATGCATAAARACTTCCTATTAAAATAAGCT
TTGGRAGAGATT

FIG. 15

>15088
MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSADCSELGLSAVPGDLDPLTAYLDLSMNNLT
ELQPGLFHLRFLEELRLSGNHLSHIPGQAFSGLYSLKIIMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSF
EGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQHLGTHSFEGLHNLE
TLDLNYNKLQEFFVAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAM
DIQEFPDLKGTTSLEILILTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFS
QLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLHDNQLTTLPLAGLGGIMLKIKGNLALSQAFSKDSFPKLRILEVP
YAYQCCPYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLIARQAENHYDQDIDELQLEMEDSKPHPSVQCSPTPGPFK
PCEYLFESWGIRLAVWAIVLLSVLCNGLIVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEY
GARWETGLGCRATGFLAVLGSEASVLLLTLAAVQCSVSVCVRAYGKSPSLGSVRAGVLGCLAIAGLAAALPLASVGEY
GASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVA
FLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQA
IVAFSDVDLILELEASEAGRPPGLETYGFPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGG
GLSGGGFQPSGLAFASHV*

FIG. 16A

protein alignment between mouse and human
> LGR6.

15088m(analysis only) - Import - complete

to: FrGcgManager_9_QBAsD4iW_ check: 8637 from: 1 to: 968

15088h(analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248

		Length:	968
Quality:	4495	Gaps:	2
Ratio:	4.653	Percent Identity:	89.855
Percent Similarity:	91.097		

Match display thresholds for the alignment(s):

```
                |  = IDENTITY
                :  = 2
                .  = 1
```

FrGcgManager_9_PBA0KgkFJ x FrGcgManager_9_QBAsD4iW_ March 15, 19101 15:24

FIG. 16B

```
1   MHSPPGLLAIWLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSA  50   Mouse
    |||||| ||||||| ||||| | ||||  |  |||||||| |||||||||||
1   MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSA  50   Human

51  DCSELGLSVVPADLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN  100
    |||||| ||| || |||||||||||||||||||||||||||| ||||||||
51  DCSELGLSAVPGDLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN  100

101 HLSHIPGQAFSGLHSLKILMLQSNQLRGIPAEALWELPSLQSLRLLDANLI  150
    |||||||| |||| |||||||||  || ||||||||||||||||||||||||
101 HLSHIPGQQAFSGLIYSLKILMLQNNQLGGIPAEALWELPSLQSLRLLDANLI  150

151 SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRH  200
    |||||||||||||||||||||||||||||||||||||||||||||  |||||
151 SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISH  200

201 IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP  250
    ||||||||||||||||||||||||| |||  || |||||||||| |||||||
201 IPDYAFQNLTSLVVLHLHNNRIQHLGTHNFEGLHNLEPLDLNYNKLQEFP  250

251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA  300
    |||||||||||||||||||||||||||||||||||||||||||||||||||
251 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA  300

301 FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEIHTLTTRAGIRLLPPGVCQQ  350
    |||| |||||||| || |||||||||||||||| |||| |||||||  |||
301 FQYILPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTTRAGIRLLPSGMCQQ  350
```

FIG. 16C

```
351 LPRLRIILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
    |||| :|||||||||||||||||||||||||| .|||| :||||||||| | =
351 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 400

401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
    ||||||||| .||: .|||||||||||||||||||||||||||||||||||
401 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450

451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF 500
    |||||||||||||||||||||||||||||| ||.|||||| :|||:|||
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 500

501 HPEEEAPKRPLGLLAGQAENHYDLDIDELQMGTEDSKPNPSVQCSPVPG 550
    | : :||. |||||| ||||||| |||||||: |||||.|||||||| | =
501 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 550

551 PFKPCBHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KIV 598
    ||||| |||||||||||||||||||||||||  ||||  ||. | |  |
551 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLITVFAGGPAPLPPVVKFV 600

599 VGAMAGANALTGISCGLLASVDALTVGQFAEYGARWESGLGCCQATGFLAV 648
    |||. |||| .|||||||||||||||||:||. |||| ||||| .|||||||
601 VGALAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV 650

649 LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA 698
    ||||||||||||||||| .||: :|:. ||||| |||||||| |||||||||
651 LGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA 700
```

FIG. 16D

```
699 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFIVVAGA 748
    |||||||||||||||||||||||||||:||||||| |||||||| |||||||
701 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFIVVAGA 750

749 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 798
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 800

799 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP 848
    ||||||||||||||||||||||||||||||||||||||||||  -   ||
801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGP 850

849 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 898
    ||||||||||||||||||||||||||||||||||||||:|||||||||||
851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 900

899 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS 948
    ||-|||| ||||- ||:-|: ||||||||| | ||||| :||-| |  -
901 LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL 950

949 SVGGALWPSGSLFASHI* 966
    | ||- ||| ||||-|-|
951 SGGGGFQPSGLAFASHV* 968
```